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APPLICATION NO.	FILING DATE	FIRST NAMED INVENTOR	ATTORNEY DOCKET NO.	CONFIRMATION NO.
10/015,715	12/12/2001	Kevin P. Baker	GNE.2830P1C56	4464

7590 05/24/2004

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EXAMINER	
LANDSMAN, ROBERT S	

ART UNIT	PAPER NUMBER
1647	

DATE MAILED: 05/24/2004

Please find below and/or attached an Office communication concerning this application or proceeding.

Office Action Summary	Application No.	Applicant(s)	
	10/015,715	BAKER ET AL.	
	Examiner	Art Unit	
	Robert Landsman	1647	

-- The MAILING DATE of this communication appears on the cover sheet with the correspondence address --

Period for Reply

A SHORTENED STATUTORY PERIOD FOR REPLY IS SET TO EXPIRE 3 MONTH(S) FROM THE MAILING DATE OF THIS COMMUNICATION.

- Extensions of time may be available under the provisions of 37 CFR 1.136(a). In no event, however, may a reply be timely filed after SIX (6) MONTHS from the mailing date of this communication.
- If the period for reply specified above is less than thirty (30) days, a reply within the statutory minimum of thirty (30) days will be considered timely.
- If NO period for reply is specified above, the maximum statutory period will apply and will expire SIX (6) MONTHS from the mailing date of this communication.
- Failure to reply within the set or extended period for reply will, by statute, cause the application to become ABANDONED (35 U.S.C. § 133). Any reply received by the Office later than three months after the mailing date of this communication, even if timely filed, may reduce any earned patent term adjustment. See 37 CFR 1.704(b).

Status

1)☐ Responsive to communication(s) filed on _____.

2a)☐ This action is **FINAL**. 2b)☒ This action is non-final.

3)☐ Since this application is in condition for allowance except for formal matters, prosecution as to the merits is closed in accordance with the practice under *Ex parte Quayle*, 1935 C.D. 11, 453 O.G. 213.

Disposition of Claims

4)☒ Claim(s) 28-47 is/are pending in the application.

4a) Of the above claim(s) _____ is/are withdrawn from consideration.

5)☐ Claim(s) _____ is/are allowed.

6)☒ Claim(s) 28-47 is/are rejected.

7)☐ Claim(s) _____ is/are objected to.

8)☐ Claim(s) _____ are subject to restriction and/or election requirement.

Application Papers

9)☒ The specification is objected to by the Examiner.

10)☒ The drawing(s) filed on 12 December 2001 is/are: a)☒ accepted or b)☐ objected to by the Examiner.

Applicant may not request that any objection to the drawing(s) be held in abeyance. See 37 CFR 1.85(a).

Replacement drawing sheet(s) including the correction is required if the drawing(s) is objected to. See 37 CFR 1.121(d).

11)☐ The oath or declaration is objected to by the Examiner. Note the attached Office Action or form PTO-152.

Priority under 35 U.S.C. § 119

12)☐ Acknowledgment is made of a claim for foreign priority under 35 U.S.C. § 119(a)-(d) or (f).

a)☐ All b)☐ Some * c)☐ None of:

1.☐ Certified copies of the priority documents have been received.

2.☐ Certified copies of the priority documents have been received in Application No. _____.

3.☐ Copies of the certified copies of the priority documents have been received in this National Stage application from the International Bureau (PCT Rule 17.2(a)).

* See the attached detailed Office action for a list of the certified copies not received.

Attachment(s)

1) ☒ Notice of References Cited (PTO-892)
2) ☐ Notice of Draftsperson's Patent Drawing Review (PTO-948)
3) ☒ Information Disclosure Statement(s) (PTO-1449 or PTO/SB/08) Paper No(s)/Mail Date 11/8/02.
4) ☐ Interview Summary (PTO-413) Paper No(s)/Mail Date. _____ .
5) ☐ Notice of Informal Patent Application (PTO-152)
6) ☒ Other: Sequence Comparisons A and B.

DETAILED ACTION

1. Formal Matters

A. The Preliminary Amendment dated 12/12/01, has been entered into the record.

B. The Preliminary Amendment dated 9/9/02, has been entered into the record.

C. The Information Disclosure Statement dated 11/8/02 has been entered into the record.

D. Claims 28-47 are pending and are the subject of this Office Action.

2. Priority

Due to the excessive number of applications from which the present application claims benefit, priority cannot be determined. However, the Examiner has concluded that the subject matter defined in this application is not supported by any of the applications in the chain of priority because the presently claimed subject matter is not supported by a specific, substantial or well-established utility, nor, for this reason, is it enabled. Accordingly, the subject matter defined in claims 28-47 has an effective filing date of 12/12/01, which is the filing date of the present application.

Should the applicant disagree with the examiner's factual determination above, it is incumbent upon the applicant to provide the serial number and specific page number(s) of any parent application filed prior to 12/12/01 which specifically supports the particular claim limitation for each and every claim limitation in all the pending claims which applicant considers to have been in possession of and fully enabled for prior to 12/12/01.

3. Information Disclosure Statement

A. All references (1 and 2) on the IDS dated 11/8/02 have been lined through since they are not in proper format, including author and accession number.

4. Specification

A. Though none could be found, due to the length of the specification, Applicants are reminded that embedded hyperlink and/or other form of browser-executable code are not permitted in the specification. See MPEP § 608.01.

B. The title of the invention is not descriptive. A new title is required that is clearly indicative of the invention to which the claims are directed. The title recites polypeptides and polynucleotides whereas the claims are drawn to polynucleotides.

5. Claim Objections

A. The syntax of claims 28-47 could be improved by replacing the phrase "shown in Figure 132 (SEQ ID NO:229)" with "of SEQ ID NO:229" and "shown in Figure 131 (SEQ ID NO:228)" with "of SEQ ID NO:228" where appropriate.

6. Claim Rejections - 35 USC § 101

35 U.S.C. 101 reads as follows:

Whoever invents or discovers any new and useful process, machine, manufacture, or composition of matter, or any new and useful improvement thereof, may obtain a patent therefor, subject to the conditions and requirements of this title.

A. Claims 28-47 are rejected under 35 U.S.C. 101 because the claimed invention is not supported by a specific, substantial and credible asserted utility or a well established utility. These claims are directed to polynucleotides homologous to SEQ ID NO:228 encoding polypeptides having various sequence homology to SEQ ID NO:229. However, the invention encompassed by these claims has no apparent or disclosed patentable utility. This rejection is consistent with the current utility guidelines, published 1/5/01, 66 FR 1092. The instant application has provided a description of an isolated protein. However, the instant application does not disclose a specific and substantial biological role of this protein or its significance.

However, it is clear from the instant specification that the claimed protein is what is termed an "orphan receptor" in the art. The instant application does not disclose the biological role of the claimed protein or its significance. Applicants disclose in the specification that the receptor has certain amino acid sequence identity to cadherins. However, homology alone is not sufficient to demonstrate utility of the present invention. There is little doubt that, after complete characterization, this protein will probably be found to have a patentable utility. This further characterization, however, is part of the act of invention and, until it has been undertaken, Applicants' claimed invention is incomplete.

The instant situation is directly analogous to that of which was addressed in Brenner v. Manson, 148 U.S.P.Q. 689 (Sus. Ct, 1966), in which a novel compound which was structurally analogous to other compounds which were known to possess anticancer activity was alleged to be potentially useful as an antitumor agent in the absence of evidence supporting this utility. The court expressed the opinion that all chemical compounds are "useful" to the chemical arts when this term is given its broadest interpretation. However, the court held that this broad interpretation was not the intended definition of "useful" as it appears in 35 U.S.C. 101, which required that an invention must have either an immediate obvious or fully disclosed "real-world" utility. The court held that:

"The basic quid pro quo contemplated by the Constitution and the Congress for granting a patent monopoly is the benefit derived by the public from an invention with substantial utility," "[u]nless and until a process is refined and developed to this point - where specific benefit exists in currently available form – there is insufficient justification for permitting an applicant to engross what may prove to be a broad field," and "a patent is not a hunting license," "[i]t is not a reward for the search, but compensation for its successful conclusion.".

The specification discloses that the polynucleotides of the invention encode proteins which have significant sequence similarity to known proteins. Based on the structural similarity, the specification asserts that the newly disclosed SEQ ID NO:228, and its encoding polynucleotides have similar activities. The assertion that the disclosed proteins have biological activities similar to known proteins cannot be accepted in the absence of supporting evidence, because generally, the art acknowledges that function cannot be predicted based solely on structural similarity to a protein found in the sequence databases. For example, Skolnick et al. (2000, Trends in Biotech. 18:34-39) state that knowing the protein structure by itself is insufficient to annotate a number of functional classes, and is also insufficient for annotating the specific details of protein function (see Box 2, p. 36). Similarly, Bork (2000, Genome Research 10:398-400) states that the error rate of functional annotations in the sequence database is considerable, making it even more difficult to infer correct function from a structural comparison of a new sequence with a sequence database (see especially p. 399). Such concerns are also echoed by Doerks et al. (1998, Trends in Genetics 14:248-250) who state that (1) functional information is only partially annotated in the database, ignoring multi functionality, resulting in underpredictions of functionality of a new protein and (2) overpredictions of functionality occur because structural similarity often does not necessarily coincide with functional similarity. Smith et al. (1997, Nature Biotechnology 15:1222-1223) remark that there are numerous cases in which proteins having very different functions share structural similarity due to evolution from a common ancestral gene.

Brenner (1999, Trends in Genetics 15:132-133) argues that accurate inference of function from homology must be a difficult problem since, assuming there are only about 1000 major gene superfamilies in nature, then most homologs must have different molecular and cellular functions. Finally, Bork et al. (1996, Trends in Genetics 12:425-427) add that the software robots that assign functions to new proteins often assign a function to a whole new protein based on structural similarity of a small domain of the new protein to a small domain of a known protein. Such questionable interpretations are written into the sequence database and are then considered facts.

Therefore, based on the discussions above concerning the specific examples of structurally similar proteins that have different functions, along with the art's recognition that one cannot rely upon structural similarity alone to determine functionality, the specification fails to teach the skilled artisan the utility of the protein of SEQ ID NO:228 which is only known to be homologous to various receptors. Therefore, the instant claims are drawn to a protein, or a polynucleotide encoding a protein which has a yet undetermined function or biological significance. There is no actual and specific significance which can be attributed to said protein identified in the specification. For this reason, the instant invention is incomplete. In the absence of a knowledge of the natural ligands or biological significance of this protein, there is no immediately obvious patentable use for it. To employ a protein of the instant invention in the identification of substances which bind to and/or mediate activity of the said receptor is clearly to use it as the object of further research which has been determined by the courts to be a non-patentable utility. Since the instant specification does not disclose a "real-world" use for said protein then the claimed invention is incomplete and, therefore, does not meet the requirements of 35 U.S.C. 101 as being useful.

The Examiner has not been able to find an assay in the specification which demonstrates a specific and substantial utility, or a well-established utility.

Furthermore, since the protein of the invention is not supported by a specific and substantial asserted utility or a well established utility, the encoding polynucleotides, vectors, host cells and methods of making proteins also lack utility.

7. Claim Rejections - 35 USC § 112, first paragraph - enablement

The following is a quotation of the first paragraph of 35 U.S.C. 112:

> The specification shall contain a written description of the invention, and of the manner and process of making and using it, in such full, clear, concise, and exact terms as to enable any person skilled in the art to which it pertains, or with which it is most nearly connected, to make and use the same and shall set forth the best mode contemplated by the inventor of carrying out his invention.

A. Claims 28-47 are rejected under 35 U.S.C. 112, first paragraph, as failing to adequately teach how to use the instant invention. Specifically, since the claimed invention is not supported by a specific, substantial and credible asserted utility or a well established utility for the reasons set forth above, one skilled in the art clearly would not know how to use the claimed invention.

B. Claims 28-47 are rejected under 35 U.S.C. 112, first paragraph, as containing subject matter which was not described in the specification in such a way as to enable one skilled in the art to which it pertains, or with which it is most nearly connected, to make and/or use the invention.

The deposit of the biological material is considered necessary for the enablement of the current invention (see MPEP Chapter 2400 and 37 C.F.R. §§ 1.801-1.809). Elements required for practicing a claimed invention must be known and readily available to the public or obtainable by a repeatable method set forth in the specification. If a deposit (203268) is made under the terms of the Budapest Treaty on the International Recognition of the Deposit of Microorganisms for the Purposes of Patent Procedure (e.g. see 961 OG 21, 1977), and Applicants, their assignee or their agent needs to provide a declaration containing the following:

1. the current address of the ATCC.
2. a declaration, or statement over attorney's signature stating that all restrictions imposed by the depositor on the availability to the public of the deposited biological material be irrevocably removed upon the granting of the patent (see MPEP Chapter 2410.01 and 37 C.F.R. § 1.808.

C. Furthermore, even if the claims possessed utility under 35 USC 101, claims 28-47 would still be rejected under 35 USC 112, first paragraph, because the specification, while then being enabling for SEQ ID NO:228 and 229, does not reasonably provide enablement for polynucleotides or polypeptides having at least 80%, 85%, 90%, 95% or 99% sequence identity to SEQ ID NO:228 or 229, to the protein encoded by ATCC No. 203268, for the extracellular domain thereof, or for vectors and host cells containing these polynucleotides. The specification does not enable any person skilled in the art to which it pertains, or with which it is most nearly connected, to make the invention commensurate in scope with these claims. There is no functional limitation in the claims. The claims encompass an unreasonable number of inoperative polypeptides, or polynucleotides which encode these polypeptides, which the skilled artisan would not know how to use.

There are no working examples of polynucleotides or polypeptides less than 100% identical to SEQ ID NO:228 or 229, or the mature form thereof (i.e. lacking its signal peptide). The skilled artisan would not know how to use non-identical polypeptides or polynucleotides on the basis of teachings in the prior art or specification unless they possessed a specific function disclosed in the instant specification, in which there is none. While the specification generally describes homologous proteins, Applicants still have not taught to which family of proteins the protein of the present invention belongs. The specification does not provide guidance for using polynucleotides encoding polypeptides related to (*i.e.*, 80%-99% identity) but not identical to SEQ ID NO:228 or 229 which do not have any specific, known function.

The claims are broad because they do not require the claimed polypeptide to be identical to the disclosed sequence and because the claims have no functional limitation.

For these reasons, which include the complexity and unpredictability of the nature of the invention and art in terms of the diversity of proteins and lack of knowledge about function(s) of encompassed polypeptides structurally related to SEQ ID NO:229, or their encoding polynucleotides (e.g. SEQ ID NO:228) the lack of direction or guidance for using polypeptides that are not identical to SEQ ID NO:229, and the breadth of the claims for structure without function, it would require undue experimentation to use the invention commensurate in scope with the claims.

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8. Claim Rejections - 35 USC § 112, first paragraph – written description

A. Claims 28-47 are rejected under 35 U.S.C. 112, first paragraph, as containing subject matter which was not described in the specification in such a way as to reasonably convey to one skilled in the relevant art that the inventor(s), at the time the application was filed, had possession of the claimed invention.

The claims are drawn to polynucleotides having at least 80%, 85%, 90%, 95% or 99% sequence identity with SEQ ID NO:228 as well as vectors and host cells. The claims do not require that the polynucleotides or encoded polypeptides of the present invention possess any particular biological activity, nor any particular conserved structure, or other disclosed distinguishing feature. Thus, the claims are drawn to a genus of polypeptides that is defined only by sequence identity.

To provide adequate written description and evidence of possession of a claimed genus, the specification must provide sufficient distinguishing identifying characteristics of the genus. The factors to be considered include disclosure of compete or partial structure, physical and/or chemical properties, functional characteristics, structure/function correlation, methods of making the claimed product, or any combination thereof. In this case, the only factor present in the claim is a partial structure in the form of a recitation of percent identity. There is not even identification of any particular portion of the structure that must be conserved. Accordingly, in the absence of sufficient recitation of distinguishing identifying characteristics, the specification does not provide adequate written description of the claimed genus.

Vas-Cath Inc. v. Mahurkar, 19USPQ2d 1111, clearly states "applicant must convey with reasonable clarity to those skilled in the art that, as of the filing date sought, he or she was in possession *of the invention.* The invention is, for purposes of the 'written description' inquiry, *whatever is now claimed.*" (See page 1117.) The specification does not "clearly allow persons of ordinary skill in the art to recognize that [he or she] invented what is claimed." (See *Vas-Cath* at page 1116). As discussed above,

the skilled artisan cannot envision the detailed chemical structure of the encompassed genus of polypeptides, and therefore conception is not achieved until reduction to practice has occurred, regardless of the complexity or simplicity of the method of isolation. Adequate written description requires more than a mere statement that it is part of the invention and reference to a potential method of isolating it. The compound itself is required. See *Fiers v. Revel*, 25 USPQ2d 1601 at 1606 (CAFC 1993) and *Amgen Inc. v. Chugai Pharmaceutical Co. Ltd.*, 18 USPQ2d 1016.

One cannot describe what one has not conceived. See *Fiddes v. Baird*, 30 USPQ2d 1481 at 1483. In *Fiddes*, claims directed to mammalian FGF's were found to be unpatentable due to lack of written description for that broad class. The specification provided only the bovine sequence.

Therefore, only isolated polypeptides comprising the amino acid sequence set forth in SEQ ID NO:229, or encoded by SEQ ID NO:228, but not the full breadth of the claims, meets the written description provision of 35 U.S.C. §112, first paragraph. Applicant is reminded that *Vas-Cath* makes clear that the written description provision of 35 U.S.C. §112 is severable from its enablement provision (see page 1115).

9. Claim Rejections - 35 USC § 112, second paragraph

The following is a quotation of the second paragraph of 35 U.S.C. 112:

> The specification shall conclude with one or more claims particularly pointing out and distinctly claiming the subject matter which the applicant regards as his invention.

Claims 28-47 are rejected under 35 U.S.C. 112, second paragraph, as being indefinite for failing to particularly point out and distinctly claim the subject matter which applicant regards as the invention.

A. Claims 28-47 are vague and indefinite since it is not clear whether or not the protein encoded by the polynucleotide of the present invention is a soluble protein (e.g protease), nor is it disclosed as being expressed on a cell surface. Accordingly, the limitation that the claimed protein comprises an "extracellular domain" is indefinite, as the art does not recognize soluble proteins as having such domains. Further, if the protein had an extracellular domain, the recitation of "the extracellular domain"..."lacking its associated signal sequence" is indefinite as a signal sequence is not generally considered to be part of an extracellular domain, as signal sequences are cleaved from said domains in the process of secretion from the cell.

B. Claims 41-43 are vague and indefinite since the claim recites "hybridizes" without the recitation of any conditions, or recites "stringent conditions: wherein these conditions are not known. Nucleic acid molecules which hybridize under conditions of "low" stringency would not necessarily hybridize under conditions of "high" stringency. Furthermore, not all conditions of "high" or "low" stringency, for example, are the same. Therefore, it is required that Applicants amend the claims to recite the exact hybridization conditions without using indefinite phrases such as "*for example*" **without adding new matter**.

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10. Claim Rejections - 35 USC § 102

The following is a quotation of the appropriate paragraphs of 35 U.S.C. 102 that form the basis for the rejections under this section made in this Office action:

> A person shall be entitled to a patent unless –
>
> (b) the invention was patented or described in a printed publication in this or a foreign country or in public use or on sale in this country, more than one year prior to the date of application for patent in the United States.

A. Claims 28-47 are rejected under 35 U.S.C. 102(b) as being anticipated by Ashkenazi et al. (WO 00/12708). The claims recite a polynucleotide at least 80% identical to that of SEQ ID NO:228 or encoding SEQ ID NO:229, as well as fragments (e.g. extracellular domains, with and without signal sequence) thereof. The claims also recite nucleic acid molecules which hybridize to SEQ ID NO:228, or one encoding SEQ ID NO:229 as well as vectors and host cells. Ashkenazi teach a polynucleotide which is 100% identical to SEQ ID NO:228 (Sequence Comparisons A) and which encodes the polypeptide of SEQ ID NO:229 (Sequence Comparison B) as well as vectors and host cells. This nucleic acid molecule will hybridize to that of the present invention even under the most stringent conditions.

11. Conclusion

A. No claim is allowable.

Advisory information

Any inquiry concerning this communication or earlier communications from the examiner should be directed to Robert Landsman whose telephone number is (703) 306-3407. The examiner can normally be reached on Monday - Friday from 8:00 AM to 5:00 PM (Eastern time) and alternate Fridays from 8:00 AM to 5:00 PM (Eastern time).

If attempts to reach the examiner by telephone are unsuccessful, the Examiner's supervisor, Gary Kunz, can be reached on (703) 308-4623.

Official papers filed by fax should be directed to (703) 308-4242. Fax draft or informal communications with the examiner should be directed to (703) 308-0294.

Any inquiry of a general nature or relating to the status of this application or proceeding should be directed to the Group receptionist whose telephone number is (703) 308-0196.

Robert Landsman, Ph.D.
Patent Examiner
Group 1600
March 21, 2004

Sequence Comparison A

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ID   AAA37087 standard; cDNA; 2848 BP.
XX
AC   AAA37087;
XX
DT   08-AUG-2000  (first entry)
XX
DE   Human PRO1340 (UNQ695) cDNA sequence SEQ ID NO:228.
XX
KW   Human; PRO polypeptide; membrane bound protein; receptor; diagnosis;
KW   transmembrane; secretion; immunoadhesion; pharmaceutical; screening; ss.
XX
OS   Homo sapiens.
XX
PN   WO200012708-A2.
XX
PD   09-MAR-2000.
XX
PF   01-SEP-1999;   99WO-US020111.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Baker K,  Goddard A,  Gurney AL,  Smith V,  Watanabe CK,  Wood WI;
XX
DR   WPI; 2000-237871/20.
DR   P-PSDB; AAY99405.
XX
PS   Claim 2; Fig 131; 773pp; English.
XX
SQ   Sequence 2848 BP; 607 A; 873 C; 828 G; 540 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 2848;  DB 3;  Length 2848;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 2848;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCTCAAGTGCCCTGCCTTGCCCCACCCAGCCCAGCCTGGCCAGAGCCCCCTGGAGAAGGA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GCTCAAGTGCCCTGCCTTGCCCCACCCAGCCCAGCCTGGCCAGAGCCCCCTGGAGAAGGA 60

Qy         61 GCTCTCTTCTTGCTTGGCAGCTGGACCAAGGGAGCCAGTCTTGGGCGCTGGAGGGCCTGT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GCTCTCTTCTTGCTTGGCAGCTGGACCAAGGGAGCCAGTCTTGGGCGCTGGAGGGCCTGT 120

Qy        121 CCTGACCATGGTCCCTGCCTGGCTGTGGCTGCTTTGTGTCTCCGTCCCCCAGGCTCTCCC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CCTGACCATGGTCCCTGCCTGGCTGTGGCTGCTTTGTGTCTCCGTCCCCCAGGCTCTCCC 180

Qy        181 CAAGGCCCAGCCTGCAGAGCTGTCTGTGGAAGTTCCAGAAAACTATGGTGGAAATTTCCC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CAAGGCCCAGCCTGCAGAGCTGTCTGTGGAAGTTCCAGAAAACTATGGTGGAAATTTCCC 240

Qy        241 TTTATACCTGACCAAGTTGCCGCTGCCCCGTGAGGGGGCTGAAGGCCAGATCGTGCTGTC 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TTTATACCTGACCAAGTTGCCGCTGCCCCGTGAGGGGGCTGAAGGCCAGATCGTGCTGTC 300

Qy        301 AGGGGACTCAGGCAAGGCAACTGAGGGCCCATTTGCTATGGATCCAGATTCTGGCTTCCT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 AGGGGACTCAGGCAAGGCAACTGAGGGCCCATTTGCTATGGATCCAGATTCTGGCTTCCT 360

Qy        361 GCTGGTGACCAGGGCCCTGGACCGAGAGGAGCAGGCAGAGTACCAGCTACAGGTCACCCT 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GCTGGTGACCAGGGCCCTGGACCGAGAGGAGCAGGCAGAGTACCAGCTACAGGTCACCCT 420
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A

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Qy        421 GGAGATGCAGGATGGACATGTCTTGTGGGGTCCACAGCCTGTGCTTGTGCACGTGAAGGA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 GGAGATGCAGGATGGACATGTCTTGTGGGGTCCACAGCCTGTGCTTGTGCACGTGAAGGA 480

Qy        481 TGAGAATGACCAGGTGCCCCATTTCTCTCAAGCCATCTACAGAGCTCGGCTGAGCCGGGG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 TGAGAATGACCAGGTGCCCCATTTCTCTCAAGCCATCTACAGAGCTCGGCTGAGCCGGGG 540

Qy        541 TACCAGGCCTGGCATCCCCTTCCTCTTCCTTGAGGCTTCAGACCGGGATGAGCCAGGCAC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 TACCAGGCCTGGCATCCCCTTCCTCTTCCTTGAGGCTTCAGACCGGGATGAGCCAGGCAC 600

Qy        601 AGCCAACTCGGATCTTCGATTCCACATCCTGAGCCAGGCTCCAGCCCAGCCTTCCCCAGA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AGCCAACTCGGATCTTCGATTCCACATCCTGAGCCAGGCTCCAGCCCAGCCTTCCCCAGA 660

Qy        661 CATGTTCCAGCTGGAGCCTCGGCTGGGGGCTCTGGCCCTCAGCCCCAAGGGGAGCACCAG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CATGTTCCAGCTGGAGCCTCGGCTGGGGGCTCTGGCCCTCAGCCCCAAGGGGAGCACCAG 720

Qy        721 CCTTGACCACGCCCTGGAGAGGACCTACCAGCTGTTGGTACAGGTCAAGGACATGGGTGA 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 CCTTGACCACGCCCTGGAGAGGACCTACCAGCTGTTGGTACAGGTCAAGGACATGGGTGA 780

Qy        781 CCAGGCCTCAGGCCACCAGGCCACTGCCACCGTGGAAGTCTCCATCATAGAGAGCACCTG 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 CCAGGCCTCAGGCCACCAGGCCACTGCCACCGTGGAAGTCTCCATCATAGAGAGCACCTG 840

Qy        841 GGTGTCCCTAGAGCCTATCCACCTGGCAGAGAATCTCAAAGTCCTATACCCGCACCACAT 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 GGTGTCCCTAGAGCCTATCCACCTGGCAGAGAATCTCAAAGTCCTATACCCGCACCACAT 900

Qy        901 GGCCCAGGTACACTGGAGTGGGGGTGATGTGCACTATCACCTGGAGAGCCATCCCCCGGG 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 GGCCCAGGTACACTGGAGTGGGGGTGATGTGCACTATCACCTGGAGAGCCATCCCCCGGG 960

Qy        961 ACCCTTTGAAGTGAATGCAGAGGGAAACCTCTACGTGACCAGAGAGCTGGACAGAGAAGC 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 ACCCTTTGAAGTGAATGCAGAGGGAAACCTCTACGTGACCAGAGAGCTGGACAGAGAAGC 1020

Qy       1021 CCAGGCTGAGTACCTGCTCCAGGTGCGGGCTCAGAATTCCCATGGCGAGGACTATGCGGC 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 CCAGGCTGAGTACCTGCTCCAGGTGCGGGCTCAGAATTCCCATGGCGAGGACTATGCGGC 1080

Qy       1081 CCCTCTGGAGCTGCACGTGCTGGTGATGGATGAGAATGACAACGTGCCTATCTGCCCTCC 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 CCCTCTGGAGCTGCACGTGCTGGTGATGGATGAGAATGACAACGTGCCTATCTGCCCTCC 1140

Qy       1141 CCGTGACCCCACAGTCAGCATCCCTGAGCTCAGTCCACCAGGTACTGAAGTGACTAGACT 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 CCGTGACCCCACAGTCAGCATCCCTGAGCTCAGTCCACCAGGTACTGAAGTGACTAGACT 1200

Qy       1201 GTCAGCAGAGGATGCAGATGCCCCCGGCTCCCCCAATTCCCACGTTGTGTATCAGCTCCT 1260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 GTCAGCAGAGGATGCAGATGCCCCCGGCTCCCCCAATTCCCACGTTGTGTATCAGCTCCT 1260

Qy       1261 GAGCCCTGAGCCTGAGGATGGGGTAGAGGGGAGAGCCTTCCAGGTGGACCCCACTTCAGG 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 GAGCCCTGAGCCTGAGGATGGGGTAGAGGGGAGAGCCTTCCAGGTGGACCCCACTTCAGG 1320

Qy       1321 CAGTGTGACGCTGGGGGTGCTCCCACTCCGAGCAGGCCAGAACATCCTGCTTCTGGTGCT 1380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 CAGTGTGACGCTGGGGGTGCTCCCACTCCGAGCAGGCCAGAACATCCTGCTTCTGGTGCT 1380
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Qy       1381 GGCCATGGACCTGGCAGGCGCAGAGGGTGGCTTCAGCAGCACGTGTGAAGTCGAAGTCGC 1440
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1381 GGCCATGGACCTGGCAGGCGCAGAGGGTGGCTTCAGCAGCACGTGTGAAGTCGAAGTCGC 1440

Qy       1441 AGTCACAGATATCAATGATCACGCCCCTGAGTTCATCACTTCCCAGATTGGGCCTATAAG 1500
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1441 AGTCACAGATATCAATGATCACGCCCCTGAGTTCATCACTTCCCAGATTGGGCCTATAAG 1500

Qy       1501 CCTCCCTGAGGATGTGGAGCCCGGGACTCTGGTGGCCATGCTAACAGCCATTGATGCTGA 1560
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1501 CCTCCCTGAGGATGTGGAGCCCGGGACTCTGGTGGCCATGCTAACAGCCATTGATGCTGA 1560

Qy       1561 CCTCGAGCCCGCCTTCCGCCTCATGGATTTTGCCATTGAGAGGGGAGACACAGAAGGGAC 1620
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1561 CCTCGAGCCCGCCTTCCGCCTCATGGATTTTGCCATTGAGAGGGGAGACACAGAAGGGAC 1620

Qy       1621 TTTTGGCCTGGATTGGGAGCCAGACTCTGGGCATGTTAGACTCAGACTCTGCAAGAACCT 1680
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Db       1621 TTTTGGCCTGGATTGGGAGCCAGACTCTGGGCATGTTAGACTCAGACTCTGCAAGAACCT 1680

Qy       1681 CAGTTATGAGGCAGCTCCAAGTCATGAGGTGGTGGTGGTGGTGCAGAGTGTGGCGAAGCT 1740
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1681 CAGTTATGAGGCAGCTCCAAGTCATGAGGTGGTGGTGGTGGTGCAGAGTGTGGCGAAGCT 1740

Qy       1741 GGTGGGGCCAGGCCCAGGCCCTGGAGCCACCGCCACGGTGACTGTGCTAGTGGAGAGAGT 1800
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Db       1741 GGTGGGGCCAGGCCCAGGCCCTGGAGCCACCGCCACGGTGACTGTGCTAGTGGAGAGAGT 1800

Qy       1801 GATGCCACCCCCCAAGTTGGACCAGGAGAGCTACGAGGCCAGTGTCCCCATCAGTGCCCC 1860
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1801 GATGCCACCCCCCAAGTTGGACCAGGAGAGCTACGAGGCCAGTGTCCCCATCAGTGCCCC 1860

Qy       1861 AGCCGGCTCTTTCCTGCTGACCATCCAGCCCTCCGACCCCATCAGCCGAACCCTCAGGTT 1920
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1861 AGCCGGCTCTTTCCTGCTGACCATCCAGCCCTCCGACCCCATCAGCCGAACCCTCAGGTT 1920

Qy       1921 CTCCCTAGTCAATGACTCAGAGGGCTGGCTCTGCATTGAGAAATTCTCCGGGGAGGTGCA 1980
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1921 CTCCCTAGTCAATGACTCAGAGGGCTGGCTCTGCATTGAGAAATTCTCCGGGGAGGTGCA 1980

Qy       1981 CACCGCCCAGTCCCTGCAGGGCGCCCAGCCTGGGGACACCTACACGGTGCTTGTGGAGGC 2040
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1981 CACCGCCCAGTCCCTGCAGGGCGCCCAGCCTGGGGACACCTACACGGTGCTTGTGGAGGC 2040

Qy       2041 CCAGGATACAGCCCTGACTCTTGCCCCTGTGCCCTCCCAATACCTCTGCACACCCCGCCA 2100
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2041 CCAGGATACAGCCCTGACTCTTGCCCCTGTGCCCTCCCAATACCTCTGCACACCCCGCCA 2100

Qy       2101 AGACCATGGCTTGATCGTGAGTGGACCCAGCAAGGACCCCGATCTGGCCAGTGGGCACGG 2160
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2101 AGACCATGGCTTGATCGTGAGTGGACCCAGCAAGGACCCCGATCTGGCCAGTGGGCACGG 2160

Qy       2161 TCCCTACAGCTTCACCCTTGGTCCCAACCCCACGGTGCAACGGGATTGGCGCCTCCAGAC 2220
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2161 TCCCTACAGCTTCACCCTTGGTCCCAACCCCACGGTGCAACGGGATTGGCGCCTCCAGAC 2220

Qy       2221 TCTCAATGGTTCCCATGCCTACCTCACCTTGGCCCTGCATTGGGTGGAGCCACGTGAACA 2280
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2221 TCTCAATGGTTCCCATGCCTACCTCACCTTGGCCCTGCATTGGGTGGAGCCACGTGAACA 2280

Qy       2281 CATAATCCCCGTGGTGGTCAGCCACAATGCCCAGATGTGGCAGCTCCTGGTTCGAGTGAT 2340
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2281 CATAATCCCCGTGGTGGTCAGCCACAATGCCCAGATGTGGCAGCTCCTGGTTCGAGTGAT 2340
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Qy       2341 CGTGTGTCGCTGCAACGTGGAGGGGCAGTGCATGCGCAAGGTGGGCCGCATGAAGGGCAT 2400
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2341 CGTGTGTCGCTGCAACGTGGAGGGGCAGTGCATGCGCAAGGTGGGCCGCATGAAGGGCAT 2400

Qy       2401 GCCCACGAAGCTGTCGGCAGTGGGCATCCTTGTAGGCACCCTGGTAGCAATAGGAATCTT 2460
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2401 GCCCACGAAGCTGTCGGCAGTGGGCATCCTTGTAGGCACCCTGGTAGCAATAGGAATCTT 2460

Qy       2461 CCTCATCCTCATTTTCACCCACTGGACCATGTCAAGGAAGAAGGACCCGGATCAACCAGC 2520
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2461 CCTCATCCTCATTTTCACCCACTGGACCATGTCAAGGAAGAAGGACCCGGATCAACCAGC 2520

Qy       2521 AGACAGCGTGCCCCTGAAGGCGACTGTCTGAATGGCCCAGGCAGCTCTAGCTGGGAGCTT 2580
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2521 AGACAGCGTGCCCCTGAAGGCGACTGTCTGAATGGCCCAGGCAGCTCTAGCTGGGAGCTT 2580

Qy       2581 GGCCTCTGGCTCCATCTGAGTCCCCTGGGAGAGAGCCCAGCACCCAAGATCCAGCAGGGG 2640
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2581 GGCCTCTGGCTCCATCTGAGTCCCCTGGGAGAGAGCCCAGCACCCAAGATCCAGCAGGGG 2640

Qy       2641 ACAGGACAGAGTAGAAGCCCCTCCATCTGCCCTGGGGTGGAGGCACCATCACCATCACCA 2700
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2641 ACAGGACAGAGTAGAAGCCCCTCCATCTGCCCTGGGGTGGAGGCACCATCACCATCACCA 2700

Qy       2701 GGCATGTCTGCAGAGCCTGGACACCAACTTTATGGACTGCCCATGGGAGTGCTCCAAATG 2760
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Db       2701 GGCATGTCTGCAGAGCCTGGACACCAACTTTATGGACTGCCCATGGGAGTGCTCCAAATG 2760

Qy       2761 TCAGGGTGTTTGCCCAATAATAAAGCCCCAGAGAACTGGGCTGGGCCCTATGGGAAAAAA 2820
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2761 TCAGGGTGTTTGCCCAATAATAAAGCCCCAGAGAACTGGGCTGGGCCCTATGGGAAAAAA 2820

Qy       2821 AAAAAAAAAAAAAAAAAAAAAAAAAAAG 2848
             ||||||||||||||||||||||||||||
Db       2821 AAAAAAAAAAAAAAAAAAAAAAAAAAAG 2848
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Sequence Comparison B

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ID   AAA37087 standard; cDNA; 2848 BP.
XX
AC   AAA37087;
XX
DT   08-AUG-2000  (first entry)
XX
DE   Human PRO1340 (UNQ695) cDNA sequence SEQ ID NO:228.
XX
PN   WO200012708-A2.
XX
SQ   Sequence 2848 BP; 607 A; 873 C; 828 G; 540 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              3.45e-288       Length:         2848
Score:                  4223.00         Matches:        807
Percent Similarity:     100.00%         Conservative:   0
Best Local Similarity:  100.00%         Mismatches:     0
Query Match:            100.00%         Indels:         0
DB:                     3               Gaps:           0

US-10-011-833A-229 (1-807) x AAA37087 (1-2848)

Qy          1 MetValProAlaTrpLeuTrpLeuLeuCysValSerValProGlnAlaLeuProLysAla 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        128 ATGGTCCCTGCCTGGCTGTGGCTGCTTTGTGTCTCCGTCCCCCAGGCTCTCCCCAAGGCC 187
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B

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Qy         21 GlnProAlaGluLeuSerValGluValProGluAsnTyrGlyGlyAsnProLeuTyr 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        188 CAGCCTGCAGAGCTGTCTGTGGAAGTTCCAGAAAACTATGGTGGAAATTTCCCTTTATAC 247

Qy         41 LeuThrLysLeuProLeuProArgGluGlyAlaGluGlyGlnIleValLeuSerGlyAsp 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        248 CTGACCAAGTTGCCGCTGCCCCGTGAGGGGGCTGAAGGCCAGATCGTGCTGTCAGGGGAC 307

Qy         61 SerGlyLysAlaThrGluGlyProPheAlaMetAspProAspSerGlyPheLeuLeuVal 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        308 TCAGGCAAGGCAACTGAGGGCCCATTTGCTATGGATCCAGATTCTGGCTTCCTGCTGGTG 367

Qy         81 ThrArgAlaLeuAspArgGluGluGlnAlaGluTyrGlnLeuGlnValThrLeuGluMet 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        368 ACCAGGGCCCTGGACCGAGAGGAGCAGGCAGAGTACCAGCTACAGGTCACCCTGGAGATG 427

Qy        101 GlnAspGlyHisValLeuTrpGlyProGlnProValLeuValHisValLysAspGluAsn 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        428 CAGGATGGACATGTCTTGTGGGGTCCACAGCCTGTGCTTGTGCACGTGAAGGATGAGAAT 487

Qy        121 AspGlnValProHisPheSerGlnAlaIleTyrArgAlaArgLeuSerArgGlyThrArg 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        488 GACCAGGTGCCCCATTTCTCTCAAGCCATCTACAGAGCTCGGCTGAGCCGGGGTACCAGG 547

Qy        141 ProGlyIleProPheLeuPheLeuGluAlaSerAspArgAspGluProGlyThrAlaAsn 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        548 CCTGGCATCCCCTTCCTCTTCCTTGAGGCTTCAGACCGGGATGAGCCAGGCACAGCCAAC 607

Qy        161 SerAspLeuArgPheHisIleLeuSerGlnAlaProAlaGlnProSerProAspMetPhe 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        608 TCGGATCTTCGATTCCACATCCTGAGCCAGGCTCCAGCCCAGCCTTCCCCAGACATGTTC 667

Qy        181 GlnLeuGluProArgLeuGlyAlaLeuAlaLeuSerProLysGlySerThrSerLeuAsp 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        668 CAGCTGGAGCCTCGGCTGGGGGCTCTGGCCCTCAGCCCCAAGGGGAGCACCAGCCTTGAC 727

Qy        201 HisAlaLeuGluArgThrTyrGlnLeuLeuValGlnValLysAspMetGlyAspGlnAla 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        728 CACGCCCTGGAGAGGACCTACCAGCTGTTGGTACAGGTCAAGGACATGGGTGACCAGGCC 787

Qy        221 SerGlyHisGlnAlaThrAlaThrValGluValSerIleIleGluSerThrTrpValSer 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        788 TCAGGCCACCAGGCCACTGCCACCGTGGAAGTCTCCATCATAGAGAGCACCTGGGTGTCC 847

Qy        241 LeuGluProIleHisLeuAlaGluAsnLeuLysValLeuTyrProHisHisMetAlaGln 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        848 CTAGAGCCTATCCACCTGGCAGAGAATCTCAAAGTCCTATACCCGCACCACATGGCCCAG 907

Qy        261 ValHisTrpSerGlyGlyAspValHisTyrHisLeuGluSerHisProProGlyProPhe 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        908 GTACACTGGAGTGGGGGTGATGTGCACTATCACCTGGAGAGCCATCCCCCGGGACCCTTT 967

Qy        281 GluValAsnAlaGluGlyAsnLeuTyrValThrArgGluLeuAspArgGluAlaGlnAla 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        968 GAAGTGAATGCAGAGGGAAACCTCTACGTGACCAGAGAGCTGGACAGAGAAGCCCAGGCT 1027

Qy        301 GluTyrLeuLeuGlnValArgAlaGlnAsnSerHisGlyGluAspTyrAlaAlaProLeu 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1028 GAGTACCTGCTCCAGGTGCGGGCTCAGAATTCCCATGGCGAGGACTATGCGGCCCCTCTG 1087
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Qy       321 GluLeuHisValLeuValMetAspGluAsnAspAsnValProIleCysProProArgAsp 340
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1088 GAGCTGCACGTGCTGGTGATGGATGAGAATGACAACGTGCCTATCTGCCCTCCCCGTGAC 1147

Qy       341 ProThrValSerIleProGluLeuSerProProGlyThrGluValThrArgLeuSerAla 360
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1148 CCCACAGTCAGCATCCCTGAGCTCAGTCCACCAGGTACTGAAGTGACTAGACTGTCAGCA 1207

Qy       361 GluAspAlaAspAlaProGlySerProAsnSerHisValValTyrGlnLeuLeuSerPro 380
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1208 GAGGATGCAGATGCCCCCGGCTCCCCCAATTCCCACGTTGTGTATCAGCTCCTGAGCCCT 1267

Qy       381 GluProGluAspGlyValGluGlyArgAlaPheGlnValAspProThrSerGlySerVal 400
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1268 GAGCCTGAGGATGGGGTAGAGGGGAGAGCCTTCCAGGTGGACCCCACTTCAGGCAGTGTG 1327

Qy       401 ThrLeuGlyValLeuProLeuArgAlaGlyGlnAsnIleLeuLeuLeuValLeuAlaMet 420
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1328 ACGCTGGGGGTGCTCCCACTCCGAGCAGGCCAGAACATCCTGCTTCTGGTGCTGGCCATG 1387

Qy       421 AspLeuAlaGlyAlaGluGlyGlyPheSerSerThrCysGluValGluValAlaValThr 440
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1388 GACCTGGCAGGCGCAGAGGGTGGCTTCAGCAGCACGTGTGAAGTCGAAGTCGCAGTCACA 1447

Qy       441 AspIleAsnAspHisAlaProGluPheIleThrSerGlnIleGlyProIleSerLeuPro 460
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1448 GATATCAATGATCACGCCCCTGAGTTCATCACTTCCCAGATTGGGCCTATAAGCCTCCCT 1507

Qy       461 GluAspValGluProGlyThrLeuValAlaMetLeuThrAlaIleAspAlaAspLeuGlu 480
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1508 GAGGATGTGGAGCCCGGGACTCTGGTGGCCATGCTAACAGCCATTGATGCTGACCTCGAG 1567

Qy       481 ProAlaPheArgLeuMetAspPheAlaIleGluArgGlyAspThrGluGlyThrPheGly 500
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1568 CCCGCCTTCCGCCTCATGGATTTTGCCATTGAGAGGGGAGACACAGAAGGGACTTTTGGC 1627

Qy       501 LeuAspTrpGluProAspSerGlyHisValArgLeuArgLeuCysLysAsnLeuSerTyr 520
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1628 CTGGATTGGGAGCCAGACTCTGGGCATGTTAGACTCAGACTCTGCAAGAACCTCAGTTAT 1687

Qy       521 GluAlaAlaProSerHisGluValValValValValGlnSerValAlaLysLeuValGly 540
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1688 GAGGCAGCTCCAAGTCATGAGGTGGTGGTGGTGGTGCAGAGTGTGGCGAAGCTGGTGGGG 1747

Qy       541 ProGlyProGlyProGlyAlaThrAlaThrValThrValLeuValGluArgValMetPro 560
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1748 CCAGGCCCAGGCCCTGGAGCCACCGCCACGGTGACTGTGCTAGTGGAGAGAGTGATGCCA 1807

Qy       561 ProProLysLeuAspGlnGluSerTyrGluAlaSerValProIleSerAlaProAlaGly 580
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1808 CCCCCCAAGTTGGACCAGGAGAGCTACGAGGCCAGTGTCCCCATCAGTGCCCCAGCCGGC 1867

Qy       581 SerPheLeuLeuThrIleGlnProSerAspProIleSerArgThrLeuArgPheSerLeu 600
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1868 TCTTTCCTGCTGACCATCCAGCCCTCCGACCCCATCAGCCGAACCCTCAGGTTCTCCCTA 1927

Qy       601 ValAsnAspSerGluGlyTrpLeuCysIleGluLysPheSerGlyGluValHisThrAla 620
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1928 GTCAATGACTCAGAGGGCTGGCTCTGCATTGAGAAATTCTCCGGGGAGGTGCACACCGCC 1987
Qy       621 GlnSerLeuGlnGlyAlaGlnProGlyAspThrTyrThrValLeuValGluAlaGlnAsp 640
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1988 CAGTCCCTGCAGGGCGCCCAGCCTGGGGACACCTACACGGTGCTTGTGGAGGCCCAGGAT 2047
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Qy        641 ThrAlaLeuThrLeuAlaProValProSerGlnTyrLeuCysThrProArgGlnAspHis 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2048 ACAGCCCTGACTCTTGCCCCTGTGCCCTCCCAATACCTCTGCACACCCCGCCAAGACCAT 2107

Qy        661 GlyLeuIleValSerGlyProSerLysAspProAspLeuAlaSerGlyHisGlyProTyr 680
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2108 GGCTTGATCGTGAGTGGACCCAGCAAGGACCCCGATCTGGCCAGTGGGCACGGTCCCTAC 2167

Qy        681 SerPheThrLeuGlyProAsnProThrValGlnArgAspTrpArgLeuGlnThrLeuAsn 700
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2168 AGCTTCACCCTTGGTCCCAACCCCACGGTGCAACGGGATTGGCGCCTCCAGACTCTCAAT 2227

Qy        701 GlySerHisAlaTyrLeuThrLeuAlaLeuHisTrpValGluProArgGluHisIleIle 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2228 GGTTCCCATGCCTACCTCACCTTGGCCCTGCATTGGGTGGAGCCACGTGAACACATAATC 2287

Qy        721 ProValValValSerHisAsnAlaGlnMetTrpGlnLeuLeuValArgValIleValCys 740
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2288 CCCGTGGTGGTCAGCCACAATGCCCAGATGTGGCAGCTCCTGGTTCGAGTGATCGTGTGT 2347

Qy        741 ArgCysAsnValGluGlyGlnCysMetArgLysValGlyArgMetLysGlyMetProThr 760
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2348 CGCTGCAACGTGGAGGGGCAGTGCATGCGCAAGGTGGGCCGCATGAAGGGCATGCCCACG 2407

Qy        761 LysLeuSerAlaValGlyIleLeuValGlyThrLeuValAlaIleGlyIlePheLeuIle 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2408 AAGCTGTCGGCAGTGGGCATCCTTGTAGGCACCCTGGTAGCAATAGGAATCTTCCTCATC 2467

Qy        781 LeuIlePheThrHisTrpThrMetSerArgLysLysAspProAspGlnProAlaAspSer 800
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2468 CTCATTTTCACCCACTGGACCATGTCAAGGAAGAAGGACCCGGATCAACCAGCAGACAGC 2527

Qy        801 ValProLeuLysAlaThrVal 807
              |||||||||||||||||||||
Db       2528 GTGCCCCTGAAGGCGACTGTC 2548
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